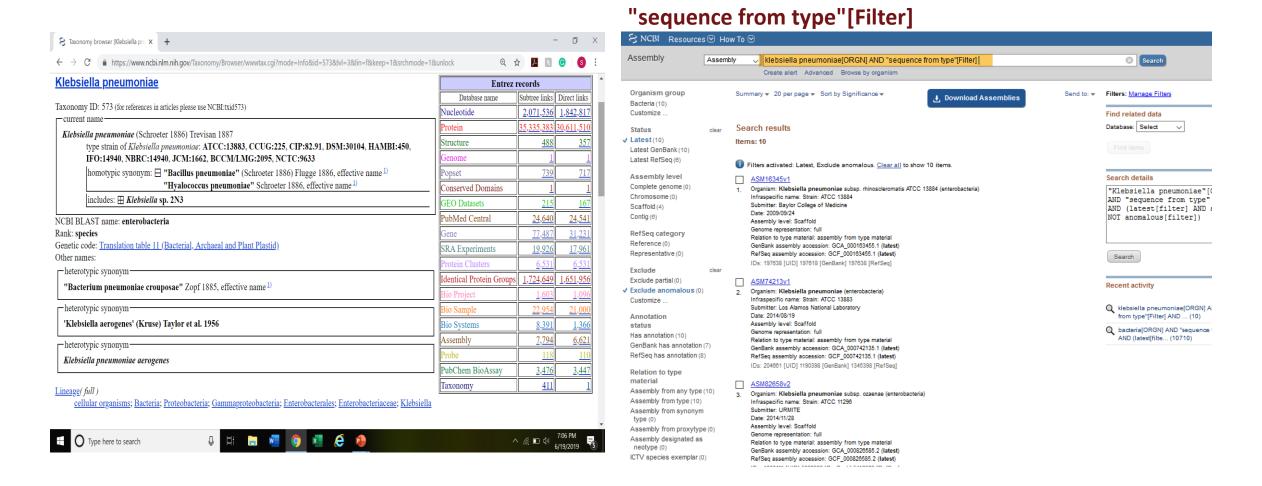
NCBI Taxonomy Database for Prokaryotic Curation

Shobha Sharma



Background: Type Strains in the NCBI Taxonomy Database







Method: Correcting Prokaryotic Genomes based on Average Nucleotide Identity (ANI)

INTERNATIONAL
JOURNAL OF SYSTEMATIC
AND EVOLUTIONARY
MICROBIOLOGY

RESEARCH ARTICLE

Ciufo et al., Int J Syst Evol Microbiol 2018;68:2386–2392 DOI 10.1099/ijsem.0.002809





Using average nucleotide identity to improve taxonomic assignments in prokaryotic genomes at the NCBI

Stacy Ciufo,* Sivakumar Kannan, Shobha Sharma, Azat Badretdin, Karen Clark, Seán Turner, Slava Brover, Conrad L. Schoch, Avi Kimchi and Michael DiCuccio

All new submissions of prokaryotic genomes to GenBank are screened using ANI to known type assemblies. (96% ANI and 80% coverage)

Public genomes in GenBank have been evaluated against all confirmed type assemblies and this evaluation process is repeated whenever a new type assembly is submitted and confirmed





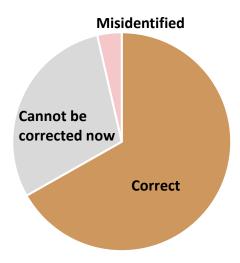
Result: Correctly Identified Genomes

GenBank gets ~1,000 prokaryotic genome submissions every week!

Since 2017, we corrected ~2,100 new submissions

~800 species IDs have been corrected for public genomes ANI method relies heavily on correctly identified type assemblies

Multiple assemblies from type are excellent resource for evaluation







Thank You!

Visit NCBI Exhibit Booth #433 for Lunch Time Demo/Talk

